

Application Serial No. 10/627,592 - Filed: July 25, 2003
Inventor: Peter B. Vander Horn - Attorney Docket No.: 020130-001420US
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Figure 1 BLOSUM62 Substitution Matrix

	C	S	Т	P	Α	G	N	D	E	Q	Н	R	K	M	I	L	V	F	Y	W
С	9	-	1	-	0	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
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			1	1			1	2	1	1	2	1	1	1	1	1	2	2	2	3
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I	-	-	-	-	-	-	-	-	-	-	1	-	-	1	4	2	1	0	-	-
	1	2	2	3	1	4	3	3	3	3	3	3	3						1	3
L	-	1	-	-	-	-	-	-	-	-	-	-	-	2	2	4	3	0	-	-
	1	2	2	3	1	4	3	4	3	2	3	2	2						1	2
V	-	-	-	-	0	-	-	-	-	-	-	-	-	1	3	1	4	- 1	-	-
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F	-	-	-	-	-	-	-	-	-	-	-	-	-	0	0	0	-	6	3	1
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Figure 2. Blast alignment of Pfu (query 1) against Deep Vent (subject 1)

>gi | 2494186 | sp | Q51334 | DPOL_PYRSD DNA polymerase (Deep Vent DNA polymerase) [Contains: Endonuclease PI-PspI (Psp-GDB pol intein)] Length = 1312Score = 816 bits (2109), Expect = 0.0 Identities = 414/493 (83%), Positives = 459/493 (92%) MILDVDYITEEGKPVIRLFKKENGKFKIEHDRTFRPYIYALLRDDSKIEEVKKITGERHG 60 Query: 1 MILD DYITE+GKP+IR+FKKENG+FK+E+DR FRPYIYALL+DDS+I+EV+KIT ERHG Sbjct: 1 MILDADYITEDGKPIIRIFKKENGEFKVEYDRNFRPYIYALLKDDSQIDEVRKITAERHG 60 Query: 61 KIVRIVDVEKVEKKFLGKPITVWKLYLEHPQDVPTIREKVREHPAVVDIFEYDIPFAKRY 120 KIVRI+D EKV KKFLG+PI VW+LY EHPQDVP IR+K+REH AV+DIFEYDIPFAKRY Sbjct: 61 KIVRIIDAEKVRKKFLGRPIEVWRLYFEHPQDVPAIRDKIREHSAVIDIFEYDIPFAKRY 120 Query: 121 LIDKGLIPMEGEEELKILAFDIETLYHEGEEFGKGPIIMISYADENEAKVITWKNIDLPY 180 LIDKGLIPMEG+EELK+LAFDIETLYHEGEEF KGPIIMISYADE EAKVITWK IDLPY Sbjct: 121 LIDKGLIPMEGDEELKLLAFDIETLYHEGEEFAKGPIIMISYADEEEAKVITWKKIDLPY 180 Query: 181 VEVVSSEREMIKRFLRIIREKDPDIIVTYNGDSFDFPYLAKRAEKLGIKLTIGRDGSEPK 240 VEVVSSEREMIKRFL++IREKDPD+I+TYNGDSFD PYL KRAEKLGIKL +GRDGSEPK Sbjct: 181 VEVVSSEREMIKRFLKVIREKDPDVIITYNGDSFDLPYLVKRAEKLGIKLPLGRDGSEPK 240 Query: 241 MQRIGDMTAVEVKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAKAWE 300 MQR+GDMTAVE+KGRIHFDLYHVI RTINLPTYTLEAVYEAIFGKPKEKVYA EIA+AWE Sbjct: 241 MQRLGDMTAVEIKGRIHFDLYHVIRRTINLPTYTLEAVYEAIFGKPKEKVYAHEIAEAWE 300 Query: 301 SGENLERVAKYSMEDAKATYELGKEFLPMEIQLSRLVGQPLWDVSRSSTGNLVEWFLLRK 360 +G+ LERVAKYSMEDAK TYELG+EF PME OLSRLVGOPLWDVSRSSTGNLVEW+LLRK Sbjct: 301 TGKGLERVAKYSMEDAKVTYELGREFFPMEAQLSRLVGQPLWDVSRSSTGNLVEWYLLRK 360 Ouery: 361 AYERNEVAPNKPSEEEYQRRLRESYTGGFVKEPEKGLWENIVYLDFRALYPSIIITHNVS 420 AYERNE+APNKP E EY+RRLRESY GG+VKEPEKGLWE +V LDFR+LYPSIIITHNVS Sbjct: 361 AYERNELAPNKPDEREYERRLRESYAGGYVKEPEKGLWEGLVSLDFRSLYPSIIITHNVS 420 Query: 421 PDTLNLEGCKNYDIAPQVGHKFCKDIPGFIPSLLGHLLEERQKIKTKMKETQDPIEKILL 480 PDTLN EGC+ YD+AP+VGHKFCKD PGFIPSLL LL+ERQ+IK KMK ++DPIEK +L Sbjct: 421 PDTLNREGCREYDVAPEVGHKFCKDFPGFIPSLLKRLLDERQEIKRKMKASKDPIEKKML 480

Query: 481 DYRQKAIKLLANS 493 DYRQ+AIK+LANS Sbjct: 481 DYRQRAIKILANS 493

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Figure 2--continued. Blast alignment of Pfu (query 1) against Deep Vent (subject 1)

Score = 473 bits (1216), Expect = e-133 Identities = 248/283 (87%), Positives = 269/283 (94%)

Query: 492 NSFYGYYGYAKARWYCKECAESVTAWGRKYIELVWKELEEKFGFKVLYIDTDGLYATIPG 551 NS+YGYYGYAKARWYCKECAESVTAWGR+YIE V KELEEKFGFKVLYIDTDGLYATIPG

Sbjct: 1029 NSYYGYYGYAKARWYCKECAESVTAWGREYIEFVRKELEEKFGFKVLYIDTDGLYATIPG 1088

Query: 552 GESEEIKKKALEFVKYINSKLPGLLELEYEGFYKRGFFVTKKRYAVIDEEGKVITRGLEI 611

+ EEIKKKALEFV YIN+KLPGLLELEYEGFY RGFFVTKK+YA+IDEEGK+ITRGLEI Sbjct: 1089 AKPEEIKKKALEFVDYINAKLPGLLELEYEGFYVRGFFVTKKKYALIDEEGKIITRGLEI 1148

Query: 612 VRRDWSEIAKETQARVLETILKHGDVEEAVRIVKEVIQKLANYEIPPEKLAIYEQITRPL 671

VRRDWSEIAKETQA+VLE ILKHG+VEEAV+IVKEV +KL+ YEIPPEKL IYEQITRPL

Sbjct: 1149 VRRDWSEIAKETQAKVLEAILKHGNVEEAVKIVKEVTEKLSKYEIPPEKLVIYEQITRPL 1208

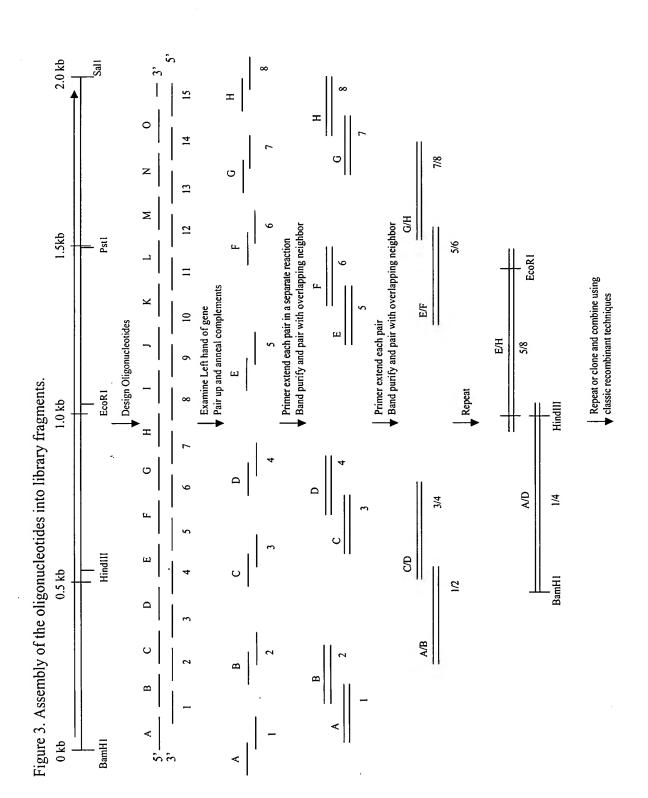
Query: 672 HEYKAIGPHVAVAKKLAAKGVKIKPGMVIGYIVLRGDGPISNRAILAEEYDPKKHKYDAE 731

HEYKAIGPHVAVAK+LAA+GVK++PGMVIGYIVLRGDGPIS RAILAEE+D +KHKYDAE Sbjct: 1209 HEYKAIGPHVAVAKRLAARGVKVRPGMVIGYIVLRGDGPISKRAILAEEFDLRKHKYDAE 1268

Query: 732 YYIENQVLPAVLRILEGFGYRKEDLRYQKTRQVGLTSWLNIKK 774

YYIENQVLPAVLRILE FGYRKEDLR+QKT+Q GLT+WLNIKK

Sbjct: 1269 YYIENQVLPAVLRILEAFGYRKEDLRWQKTKQTGLTAWLNIKK 1311



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FIG. 4

E coli dut polypeptide sequence:

 $\tt MKKIDVKILDPRVGKEFPLPTYATSGSAGLDLRACLNDAVELAPGDTTLVPTGLAIHIADPSLAAMMLPRSGLGHKHG\\ IVLGNLVGLIDSDYQGQLMISVWNRGQDSFTIQPGERIAQMIFVPVVQAEFNLVEDFDATDRGEGGFGHSGRQ$

AAD polypeptide sequence:

MSKVILKIKRLPHAQDLPLPSYATPHSSGLDLRAAIEKPLKIKPFERVLIPTGLILEIPEGYEGQVRPRSGLAWKKGL TVLNAPGTIDADYRGEVKVILVNLGNEEVVIERGERIAQLVIAPVQRVEVVEVEEVSQTQRGEGGFGSTGTK

Alignment:

Identities = 61/149 (40%), Positives = 91/149 (60%), Gaps = 1/149 (0%)

Query: 1 MKKIDVKILDPRVGKEFPLPTYATSGSAGLDLRACLNDAVELAPGDTTLVPTGLAIHIAD 60 M K+ +KI ++ PLP+YAT S+GLDLRA + +++ P + L+PTGL + I +

Sbjct: 1 MSKVILKIKRLPHAQDLPLPSYATPHSSGLDLRAAIEKPLKIKPFERVLIPTGLILEIPE 60

Query: 61 PSLAAMMLPRSGLGHKHGIVLGNLVGLIDSDYQGQLMISVWNRGQDSFTIQPGERIAQMI 120

+ PRSGL K G+ + N G ID+DY+G++ + + N G + I+ GERIAQ++
Sbjct: 61 -GYEGQVRPRSGLAWKKGLTVLNAPGTIDADYRGEVKVILVNLGNEEVVIERGERIAQLV 119

Query: 121 FVPVVQAEFNLVEDFDATDRGEGGFGHSG 149

PV + E VE+ T RGEGGFG +G

Sbjct: 120 IAPVQRVEVVEVEVSQTQRGEGGFGSTG 148

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ACG ACT ACA

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ATT ATC ATA

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GTG GTT GTC GTA

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GCC GCC GCA GCT

CGC TTA CGC TTA CGG TTG CGA CTT AGA CTC

CTG TTA TTG CTT CTC

AGC TCT AGT TCA TCC TCC

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S AGC TCT AGT TCA TCA

GGC GGT GGG GGA

A GCG GCC GCA GCA

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T ACC ACG ACT ACT

A GCG GCC GCA GCA GCT

T ACC ACG ACT ACT

YTAT TAC

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5A.	5A. Aligned parental sequence showing all possible codons	ı pa	arei	ntal	l se	gue	nce	sho	wing	J al	J Ď	ວຮຮ່	ible	00	don	Ø						
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the removal of non-similar degeneracies; selection of ADD parent 5C. A minimal encoding sequence after residues at particular sites

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D GAT GAC	e Gag Gag			ОM		GAT A	ΩШ
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5A--continued

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FIGURE 6

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70	CCG GGC P	CTG GAC L	CCG GGC P	T(G,	/G) C /C) G /S	TAT ATA Y	GCG CGC A	ACC TGG T	(A/	C) CT G) GA /P	CAC GTG H	AGC TCG S	(C/.	T) CA	GGC CCG G	CTG GAC L	GAT CTA D	CTG GAC L	113
114	CGT	GCG	(T/C	G) (G,	/c)c	(C/ <i>P</i>	YT (A	(A/0	3) A (0	C/G)	(A/	G) A (I	(A)	(G/	C) CG	(G/0	C) TG	(G/ <i>I</i>	AA (A
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237			(G/:		A/C)		(T/I	A) AT	(C/		/G) C	(C/0 (G/0 L/) AC						266
							· ~ \ ~	Cla		12.11		(a) a	~		0/2	(a) a	222		
267	(C/G		/G) C		(G/I		'G) C			(T/C		/C)C /G)G /G			G(T				296
297		TT ((G/0			T) C	(T/C		T(C		(C/	C)TG G)AC /L			G(C				326
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357		AT T) AC	(T/C		(A/'		C(A	/C) G /G) C /A			(C/C		/T) C		389
390		'C) C	C (G,				:) AA	(T/C		/A) A	(G/	G) (T/ C) (A/ /E/Q/	T) C			CT (416
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459 GGC A(G/C)A (C/A)AG TAA TGA GGATCC GAATTC TT CCG T(C/G)T (G/T)TC ATT ACT CCTAGG CTTAAG AA

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Figure 7

10	20	30	40	50	60	70
TTGGTACCAAGCTI						
AACCATGGTTCGAA						
AACCAIGGIICGAA	GIAIACIIKI	IIIIAAINASA	CITITAAN	CGCAGACGSAG	IACSGRIIC	INAANGG
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80	90		110	120		140
GCTGCCGASCTATG						
CGACGGCTSGATAC	GCTGGRGAGI	GTCGMGTCCC	GACCTAGAC	GCACGCMSGKA	AYTSYTWSG	CSACYTT
						010
150	160	170		190	200	210
MTTRMGCCGKKTGA						
KAAYKCGGCMMACI	WISCYRCGAC	CYAAGGCTGGC	CCAGACTAGK	AASTWTAASGC	CTWCCAAKA	CKCCSCG
220	230	240		260		280
AGRTGCKGCCGCGI	AGCGGCCTGG	SCTGGAAAM	AKGGCWTARY	GSTGCTGAACG	CGSYGGGCM	YG <u>ATCGA</u>
TCYACGMCGGCGCA	TCGCCGGACC	CSGACCTTTKT	TMCCGWATYR(CSACGACTTGC	GCSRCCCGK	RC <u>TAGCT</u>
290	300	310	320	330	340	350
TRSCGATTATCRGG	GCSAASTGAV	GRTTAKCST	GTGAACCKG	GGCMASGAWGA	AKTTRYGAT	TSAGCSG
AYSGCTAATAGYCC	CCGSTTSACT	VCYAATMGSA(CACTTGGMC	CCGKTSCTWCT	TMAAYRCTA	ASTCGSC
-						
360	370	380	390	400	410	420
GGCGAACGTATTGC	GCAGMTGRTT	TWTTGYGCCGC	TGSWGCRGG	YGGAAKTTRWT	SWGGTGGAA	GAWKTTT
CCGCTTGCATAACG	CGTCKACYA	WAACRCGGC	CACSWCGYCC	RCCTTMAAYWA	SWCCACCTT	CTWMAAA
430	440	450	460	470	480	
CTCAGACCSAKCGI	GGCGAAGGCG	GCTTTGGCT	CTASCGGCAS	AMAGTAATGAG	GATCCGAAT	TCTT
GAGTCTGGSTMGCA						
						

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Figure 8.

14

atg atc ctg gat g(t/c)t gac tac atc act gaa ga(a/c) ggc aaa ccg (g/a)tt atc cgt (c/a)t(g/c) ttc
M I L D V/A D Y I T E E/D G K P V/I I R L/I/M F

aaa aaa gag aac ggc (a/g)aa ttt aag (a/g)tt gag (c/t)at gat cgc a(a/c)c ttt cgt cca tac att tac gct K K E N G K/E F K I/V E H/Y D R N/T F R P Y I Y A

ctg ctg a(g/a)a gat gat tct (a/c)ag att ga(g/t) gaa gtt a(g/a)a aaa atc act g(g/c)t gag cgc cat ggc aag att

L L R/K D D S K/Q I E/D E V K/R K I T G/A E R H G K I

214 215

gtt cgt atc (a/g)tt gat g(t/c)g gaa aag gta (g/a)(g/a)g aag aaa ttt ctg ggc a(a/g)a cca atc (a/g)(a/c)g V R I I/V D V/A E K V G/E/R/K K K F L G K/R P I K/T/E/A

gtg tgg a(g/a)a ctg tat (c/t)tc gaa cat cca caa gat gtt ccg a(t/c)t att cgc ga(g/t) aaa (g/a)tt cgc V W K/R L Y L/F E H P Q D V P T/A I R E/D K V/I R

gaa cat (c/t)ct gca gtt (g/a)tt gac atc ttc gaa tac gat att cca ttt gca aag cgt tac ctc atc gac aaa E H P/S A V V/I D I F E Y D I P F A K R Y L I D K

ggc ctg ata cca atg gag ggc ga(g/t) gaa gaa ctc aag (a/c)tc ctg gcg ttc gat ata gaa acc ctc tat G L I P M E G E/D E E L K I/L L A F D I E T L Y

cac gaa ggc gaa gag ttt g(g/c)t aaa ggc cca att ata atg att agc tat gca gat gaa (a/g)a(a/c) gaa gca aag H E G E E F G/A K G P I I M I S Y A D E <math>K/N/E/D E A

gtg att act tgg aaa aa(a/c) ata gat ctc cca tac gtt gag gtt gta tct tcc gag cgc gag atg att aag cgc v I T w K K/N I D L P Y V E V V S S E R E M I K R

ttt ctc a(g/a)a (g/a)tt atc cgc gag aag gat ccg gac (g/a)tt atc (g/a)tt act tat aac ggc gac tct ttt F L R/k V/I I R E K D P D V/I I V/I T Y N G D S F

gac (c/t)tc cca tat ctg g(t/c)g aaa cgc gca gaa aaa ctc ggt att aaa ctg (a/c)ct (a/c)tc ggc cgt gat ggt D F P Y L V/A K R A E K L G I K L T/P I/L G R D G

tcc gag ccg aag atg cag cgt (a/c)tc ggc gat atg acc gct gta gaa (g/a)tt aag ggt cgt atc cat ttc gac S E P K M Q R I/L G D M T A V E V/I K G R I H F D

ctg tat cat gta att (a/c)(c/g)c cgt act att aac ctc ccg act tac act ctc gag gct gta tat gaa gca att L Y H V I T/S/P/R R T I N L P T Y T L E A V Y E A I

ttt ggt aag ccg aag gag aag gta tac gcc (g/c)at gag att gca (a/g)ag gcg tgg gaa (a/t)cc ggt (a/g)ag F G K P K E K V Y A D/H E I A K/E A W E T/S G K/E

(a/g)(a/g)c ctc gag cgt gtt gca aaa tac tcc atg gaa gat gca aag g(t/c)g act tat gaa ctc ggc a(g/a)a gaa ttc N/G/D/S L E R V A K Y S M E D A K V/A T Y E L G R/K E F

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(c/t)tc cca atg gaa (a/g)(t/c)t cag etc tct cgc ctg gtt ggc caa cca ctg tgg gat gtt tct cgt tct tcc Q L S RLVGQPLWDVS P M E I/T/V/A acc ggt aac ctc gta gag tgg t(t/a)t ctc ctg cgc aaa gcg tac gaa cgc aac gaa (g/c)tg gct ccg aac aag VEW F/Y L L R K A Y E R N E v/t. Α cca (t/g)(c/a)c gaa (c/g)(g/a)a gag tat (c/g)aa ege egt ete ege gag tet tae (a/g)ct ggt gge t(t/a)tQ/E R R L R E S Y P S/Y/A/D R/Q/G/E E Y T/A gtt aaa gag cca gaa aag ggc ctc tgg gaa (a/g)(a/g)c (a/c)tc gtg t(c/a)c ctc gat ttt cgc (g/t)ct ctg N/S/D/G I/L v Y/S K G L W E L D tat ccq tct att atc att acc cac aac gtg tct ccg gat act ctc aac c(t/g)c gag ggc tgc a(g/a)a s P D T L N L/R E т н N V (a/g)a(a/c) tat gat (g/a)tt gct ccg (c/g)aa gta ggc cac aag ttc tgc aag gac (a/t)tc ccg ggc ttt att K/N/E/D V/I A P Q/E V G H K F C K D I/F P ccg tct ctc ctg (a/g) (a/g)g c(a/g)t ctg ctc ga(g/t) gaa cgc caa (a/g)ag att aag (a/c)(g/c)c aaa atg aag K/R/E/G R/H L L E/D E R Q K/E I K T/S/P/R K g(a/c)g(a/t)cc(c/a)ag gat ccg att gaa aaa a(t/a)a(a/c)tg ctc gac tat cgc caa a(g/a)a gcg att aaa Q/K D P I E K I/K M/L L D Y R Q R/K (a/c)tc ctc gca aac tct t(a/t)t tac ggc tat tat ggc tat gca aaa gca cgc tgg tac tgt aag gag tgt gct N S F/Y YGYYGYAKARW у с к T./T gag too gtt act got tgg ggt ogc (a/g)aa tac atc gag (c/t)tc gtg (t/c)gg aag gag otc gaa gaa aag ttt ggc E K/E Y I E L/F W/R K Ε K R L ttt aaa gtt ctc tac att gac act gat ggt ctc tat gcg act att ccg ggt g(g/c)t (a/g)ag (c/t)ct gag Y I D T D G L Y A T I P G G/A 1696 gaa att aag aaa aag got oto gaa tit gig aaa tac att aac (g/t)cg aag oto oog ggt oto oig gag oto gaa F V K(D) Y I N A/S K L P G L E tat gaa ggc ttt tat (g/a) (t/a)g cgc ggc ttc ttc gtt acc aag aag a(g/a)a tat gcg (g/c)tg att gat gaa gaa V/L G F Y V/E/M/K R G F F V T K K R/K Y A ggc aaa (g/a)tt att act cgt ggt ctc gag att gtg cgc cgt gat tgg agc gaa att gcg aaa gaa act caa gct G T. т R D W a(g/a)a gtt ctc gag (a/g)ct att ctc aaa cac ggc (g/a)ac gtt gaa gaa gct gtg a(g/a)a att gta aaa gaa gta T/A I L K H G D/N v E E A V R/K Ι a(t/c)c (c/g)aa aag ctc (g/t)ct aa(a/c) tat gaa att ccg cca gag aag ctc g(t/c)g att tat gag cag att EIPPEKL V/A I Y E I/T Q/E K L A/S K/N Y act ege eeg etg cat gag tat aag geg att ggt eeg cac gtg get gtt gea aag a(g/a)a etg get get a(g/a)a gge gtg YKAIGP Н VAVAK R/K H E aaa (g/a)tt a(g/a)a ccg ggt atg gta att ggc tac att gta ctc cgc ggc gat ggt ccg att agc aa(a/c) cgt gca P G M V I G Y I V L R G D G PIS K/N

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act a(g/a)a cag (g/a)(t/c)t ggc ctc act (g/t)ct tgg ctc aac att aaa aaa tcc ggt acc cac tag tgc tag cat gac T K/R Q V/A/I/T G L T A/S W L N I K K S G T H *

Figure 9. A comparison of the polymerase to 3' to 5' exonuclease activity

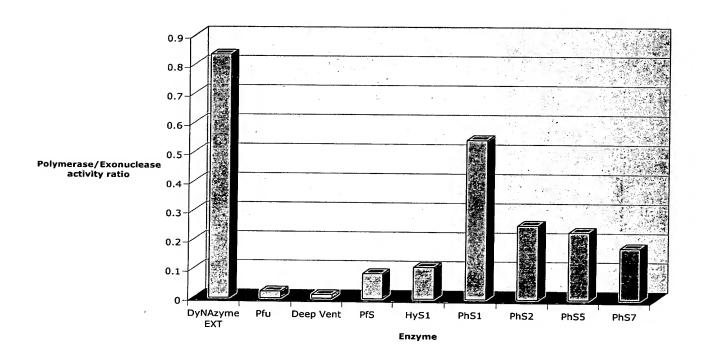
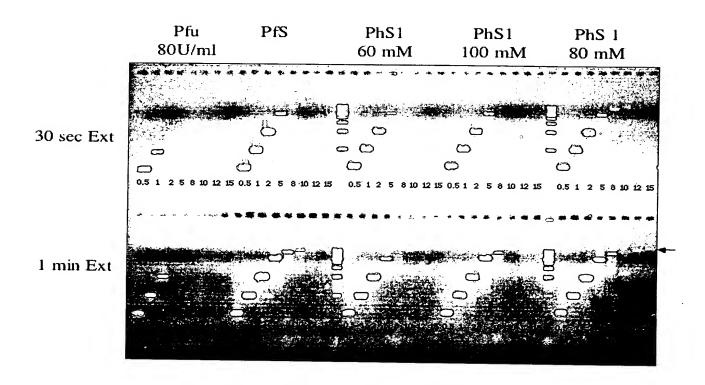


FIGURE 10



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11 E T L Y H E G E E F G K G P I I M I S Y I E T L Y H E G E E F G K G P I I M I S Y I E T L Y H E G E E F G K G P I I M I S Y I E T L Y H E G E E F G K G P I I M I S Y I E T L Y H E G E E F G K G P I I M I S Y I E T L Y H E G E E F G K G P I I M I S Y I E T L Y H E G E E F G K G P I I M I S Y I E T L Y H E G E E F G K G P I I M I S Y I E T L Y H E G E E F G K G P I I M I S Y I E T L Y H E G E E F G K G P I I M I S Y I E T L Y H E G E E F G K G P I I M I S Y I E T L Y H E G E E F G K G P I I M I S Y I E T L Y H E G E E F G K G P I I M I S Y I E T L Y H E G E E F G K G P I I M I S Y I E T L Y H E G E E F G K G P I I M I S Y I E T L Y H E G E E F G K G P I I M I S Y I E T L Y H E G E E F G K G P I I M I S Y I E T L Y H E G E E F G K G P I I M I S Y	210 D P D I I V T Y N G D S F D F P Y L A K R D P D D I I T Y N G D S F D L P Y L V K R D P D D I I T Y N G D S F D L P Y L V K R D P D I I V T Y N G D S F D L P Y L A K R C D P D V I V T Y N G D S F D L P Y L A K R C D P D V I V T Y N G D S F D L P Y L A K R C D P D I I T Y N G D S F D L P Y L A K R C D P D I I I T Y N G D S F D L P Y L A K R C D P D I I T Y N G D S F D L P Y L A K R C D P D I I T Y N G D S F D F P P Y L A K R C D P D I I T Y N G D S F D F P P Y L A K R C D P D I I T Y N G D S F D F P P P Y L A K R C D P D I I T Y N G D S F D F P P P Y L A K R C D P D I I T Y N G D S F D F P P P Y T A K R C D P P T Y T Y N G D S F D F P P P T Y T Y N G D S F D F P P P T Y T Y N G D S F D F P P P P T Y T Y N G D S F D F P P P P T Y T Y N G D S F D F P P P P T Y T Y N G D S F D F P P P P T Y T Y N G D S F D F P P P P T Y T Y N G D S F P P P P P T Y T Y N G D S F P P P P P P P P P P P P P P P P P P
KGLIPMEGEEELKILAFD KGLIPMEGDEELKLLAFD KGLIPMEGNEELKNLAFD KGLIPMEGEEELKNLAFD KGLIPMEGEEELKLLAFD KGLIPMEGEEELKLLAFD KGLIPMEGEEELKLLAFD KGLIPMEGEEELKLLAFD KGLIPMEGEEELKLLAFD KGLIPMEGEEELKILAFD KGLIPMEGEEELKILAFD KGLIPMEGEEELKILAFD KGLIPMEGEEELKILAFD KGLIPMEGEEELKILAFD	189 190 190 190 190 190 190 190
Pfu	Pfu DeepVent Hybrid_design VEV Hyb2 Hyb3 Hyb3 Hyb3 Hyb3 Hyb3 Hyb3 Hyb3 Hyb3

i I	250 280 280 280 280 280 280 280 280 280 28
Pfu DeepVent	QRIGDMIAVEVKGRIHFDLYHVINRTINLPTYTLEAVYEAIFGKPKEKVYA QRLGDMIAVETKGRIHFDLYHVINRTINLPTYTLEAVYEAIFGKPKEKVYA
Hybrid_design HvS1	QRXGDMTAVEXKGRIHFDLYHVIXRTINLPTYTLEAVYEAIFGKFKEKVYA <u>XK</u> IAXAW QRLGDMTAVEVKGRIHFDLYMVISRTINLPTYTLEAVYEAIFGKPKEKVYADDIAEAW
Hyb2	QRICDMTAVEVKGRIHFDLYHVISRTINLPTYTLEAVYEAIFGKPKEKVYADEIAGAW
Hyb3	QRLGDMTAVEVKGRIHFDLYHVISRTINLPTYTLEAVYEAIFGKPKEKVYADEIAGAW
HyS4	KLGDMIAVEVKGRIHFDLYHVISKIINLPIYILEAVYEAIFGRFKEKVYADEIAGAW RIGDMIAVEVKGRIHFDLYHVIRRIINLPTYTLEAVYEAIFGKPKEKVYADEIAKAW
PhS2	QRIGDMTAVEVKGRIHFDLYHVIRRTINLPTYTLEAVYEAIFGKPKEKVYAHEIAEAW
PhS3	O BI GRATAUFIERI VICELVERI VICELVII I DE TINI BAVALEA VVEATERV DE EVVVANOETANOM
Phys	ORIGOMTAVETRGRIHFDLYHVITRT
PhS6	RIGDMTAVE IKGRIHFD LYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAEAW
PhS7	RIGDMTAVEIKGRIHFDLYHVITRTINLPTYTLEAVYEAIFGKPKEKVYADEIAEAW
	340 350
Pfu	GENLERVAKY SMEDAKATY ELGKEFLPMEI OLS RLVGOPLWDVS RS STGNLVEWFLLR
DeepVent	TGKGLERVAKYSMEDAKVTYELGREFFFPMEAQLSRLVGQPLWDVSRSSTGNLVEWYLLRK
hybrid_design HvS1	GRALERVAKYSMEDAKATYELGKEFLPMEAOLSRLVGOPLWDVSRSSTGNLVEWVLLR
Hyb2	GEDLERVAKY SMEDAKATIYELGKEFIFIPMEVQLIPIRLVGQPLWDVSRSSTGNLVEWLLLR
Hyb3	GEDLERVAKYSMEDAKAIIYELGKEFFPMEVQLPRLVGOPLWDVSRSSTGNLVEWLLR
HyS4	GEDLERVAKYSMEDAKAIIYELGKEFIFIPMEVQLIPIRLVGQPLWDVSRSSTGNLVEWLLLR
PhS1	GEGLERVARYSMEDAKATYELGKEFFPMEAQLSKLVGQPLWDVSKSSTGNLVEWFLLR
PhS2	G EGLERVARY SMEDAKATY ELGKEF FPME I QLSKLVGQP LWDV SKSSTGNLV EWFLLK
PhS3	GERGIERVAKYSMEDAKIVITYELGKEFILIPMEHOLSRLVGOPLWDVSRSSTGNLVEWIFILLR
PhS5	LERVAKYSMEDAKATYELGKEFLPME
PhS6	GKNLERVAKYSMEDAKATYELGKEFLPME I QLSRLVGQPLWDVSRSSTGNLVEWYLLR
PhS7	K N L E R V A K Y S M E D A K A T Y E L G K E F L P M E I Q L S R L V G Q P L W D V S R S S T G N L V E W Y L L R

150 170 170 170 170 170 170 170	YVKEPEKGLWENI VSLDFRSLYPSIIITHNVS YVKEPEKGLWENLVSLDFRALYPSIIITHNVS YVKEPEKGLWENLVSLDFRALYPSIIITHNVS YVKEPEKGLWENLVSLDFRALYPSIIITHNVS	FIPSLLGHLLEERQKIKTKMKETQDPIEKILL FIPSLLKRLLDERQEIKRRMKASKDPIEKILL FIPSLLXXLLXERQXIKXXKNKASKDPIEKKML FIPSLLXXLLXERQXIKXXKNDPIEKKML FIPSLLGHLLEERQEIKTKMKETXNDPIEKILL FIPSLLGHLLEERQEIKTKMKETXDPIEKILL FIPSLLGHLLEERQEIKTKMKETXDPIEKILL FIPSLLGHLLEERQKIKRKMKASKDPIEKILL FIPSLLGHLLEERQKIKRKMKASKDPIEKKML FIPSLLKHLLDERQKIKRKMKASKDPIEKKML FIPSLLKHLLDERQKIKRKMKASKDPIEKKML FIPSLLKHLLDERQKIKRKMKATN
Pfu AYERNEVAPNKPDEREYORRIRESYTGG Hybrid_design AYERNEVAPNKPNEREYERERESYAGG Hyb2 AYERNEVAPNKPYEREYEYRRESYNGG Hyb3 AYERNELAPNKPAEQEYERRLRESYTGG Hyb3 AYERNELAPNKPAEQEYERRLRESYTGG Hyb3 AYERNELAPNKPAEQEYERRLRESYTGG Hyb3 AYERNELAPNKPAEQEYERRLRESYTGG Hyb3 AYERNELAPNKPAEQEYERRLRESYTGG PhS1 AYERNELAPNKPAEQEYERRLRESYTGG PhS1 AYERNELAPNKPAEQEYERRLRESYTGG	AYERNEVAPNKPDEEEYERLRESYAGG AYERNEVAPNKPDEEEYERLRESYTGG AYERNEVAPNKPDEEEYERLRESYTGG	PDTLNLEGCKNYDIAPQVGHKFCKDIPG PDTLNREGCREYDVAPEVGHKFCKDFPG Q_design PDTLNREGCXXYDXAPXVGHKFCKDFLG PDTLNREGCKDYDIAPEVGHKFCKDFLG PDTLNREGCKDYDIAPEVGHKFCKDFLG PDTLNREGCKDYDIAPEVGHKFCKDFLG PDTLNREGCKNYDVAPEVGHKFCKDFLG PDTLNREGCKNYDVAPEVGHKFCKDIPG PDTLNREGCKNYDIAPQVGHKFCKDIPG PDTLNREGCKNYDIAPQVGHKFCKDFPG PDTLNREGCKNYDIAPQVGHKFCKDFPG PDTLNREGCKNYDIAPQVGHKFCKDFPG
Pfu DeepVent Hybrid_d Hyb2 Hyb3 Hyb3 Hyb3 PhS1	PhS3 PhS4 PhS5 PhS6 PhS6	Pfu DeepVent Hybrid_d Hyb2 Hyb3 Hyb3 PhS1 PhS2 PhS3 PhS6 PhS6

Pfu DeepVent Hybrid_design HyS1 Hyb3 HyS4 PhS1 PhS2 PhS3 PhS5 PhS6 PhS5	IVERDWSEI IVERDWSEI IVERDWSEI IVERDWSEI IVERDWSEI IVERDWSEI IVERDWSEI IVERDWSEI IVERDWSEI IVERDWSEI IVERDWSEI IVERDWSEI	KETQARVLETIL KETQARVLEAIL KETQARVLEAIL KETQARVLEAIL KETQARVLEAIL KETQARVLEAIL KETQARVLEAIL KETQARVLEAIL KETQARVLETIL KETQARVLETIL KETQARVLETIL KETQARVLETIL	KHGDVEEAVRIVKI KHGNVEEAVKIVKI KHGNVEEAVKIVKI KHGNVEEAVKIVKI KHGNVEEAVKIVKI KHGNVEEAVKIVKI KHGNVEEAVKIVKI KHGNVEEAVKIVKI KHGNVEEAVKIVKI KHGNVEEAVKIVKI KHGNVEEAVKIVKI	EVIOKLANYEIPPEK EVXXKLIXXYEIPPEK EVXXKLIXXYEIPPEK EIIEKLAKYEIPPEK EIIEKLAKYEIPPEK EIIEKLAKYEIPPEK EVTQKLSKYEIPPEK EVTQKLSKYEIPPEK EVTQKLAKYEIPPEK EVTQKLAKYEIPPEK
Pfu DeepVent Hybrid_design Hyb3 Hyb3 Hys4 PhS2 PhS3 PhS4 PhS5	LA I Y E Q I T R P L H E Y K A I G P L X I Y E Q I T R P L H E Y K A I G P L A I Y E Q I T R P L H E Y K A I G P L A I Y E Q I T R P L H E Y K A I G P L A I Y E Q I T R P L H E Y K A I G P L A I Y E Q I T R P L H E Y K A I G P L A I Y E Q I T R P L H E Y K A I G P L A I Y E Q I T R P L H E Y K A I G P L A I Y E Q I T R P L H E Y K A I G P L A I Y E Q I T R P L H E Y K A I G P	PHVAVAKKLAAKGVK PHVAVAKKLAARGVK PHVAVAKKLAARGVK PHVAVAKKLAARGVK PHVAVAKKLAARGVK PHVAVAKKLAARGVK PHVAVAKKLAARGVK PHVAVAKKLAARGVK PHVAVAKRLAARGVK PHVAVAKRLAARGVK PHVAVAKRLAARGVK	G Y V C C C C C C C C C	RGDGPISNRAILAEE RGDGPISNRAILAEE RGDGPISKRAILAEE RGDGPISKRAILAEE RGDGPISNRAILAEE RGDGPISNRAILAEE RGDGPISNRAILAEE RGDGPISNRAILAEE

Pfu DeepVent Hybrid_design Hyb2 Hyb3 Hyb3 PhS1 PhS1	D F K K H K Y D A E Y Y I E N Q V D K K H K Y D A E Y Y I E N Q V D X X K H K Y D A E Y Y I E N Q V D K K H K Y D A E Y Y I E N Q V D L R K H K Y D A E Y Y I E N Q V D L R K H K Y D A E Y Y I E N Q V D L R K H K Y D A E Y Y I E N Q V D F K H K Y D A E Y Y I E N Q V D F K H K Y D A E Y Y I E N Q V D R K H K Y D A E Y Y I E N Q V D R K H K Y D A E Y Y I E N Q V D R K H K Y D A E Y Y I E N Q V D L K K H K Y D A E Y Y I E N Q V D L K K H K Y D A E Y Y I E N Q V	740 P A V L R I L E P A V L R I L E P A V L R I L E P A V L R I L E P A V L R I L E P A V L R I L E P A V L R I L E P A V L R I L E P A V L R I L E P A V L R I L E	FGYRKEDLR FGYRKEDLR FGYRKEDLR FGYRKEDLR FGYRKEDLR FGYRKEDLR FGYRKEDLR FGYRKEDLR	TROOKGE TROOKGE TROOKGE TROOKGE TROOKGE	1 K K S G T G G I K K S G T G G G I K K S G T G G G G G G G G G G G G G G G G G	
PhS4 PhS5 PhS6 PhS7	YDPKKHKYDAEYYIENQVLP YDLKKHKYDAEYYIENQVLP YDLKKHKYDAEYYIENQVLP	44 4	FGYRKEDLRY FGYRKEDLRY FGYRKEDLRY	RWQKTKQVGLTA RWQKTKQVGLTS RWQKTKQVGLTS	VLRILEAFGYRKEDLRWQKTKQVGLTAWLNIKKSGTGG VLRILEAFGYRKEDLRWQKTKQVGLTSWLNIKKSGTGGG VLRILEAFGYRKEDLRWQKTKQVGLTSWLNIKKSGTGGG	
Pfu	790	009	810	950	830 840	_
DeepVent Hybrid_design HyS1 Hyb2	N H D G A T V K F K Y K G E E K E V D I S K	KIKKVWRVGKM	ISFTYDEG	GGKTGRGAVSE	EKDAPKELLQMLE	
Hyb3 Hys4 PhS1	GATVKFKYKGEEKEVDISK GATVKFKYKGEEKEVDISK GATVKFKYKGEEKEVDISK	I K K V W R V G I K K V W R V G I K K V W R V G	ISFTYDEG ISFTYDEG ISFTYDEG	GGKTGRGAVSE GGKTGRGAVSE GGKTGRGAVSE	KDAPKELLOMLE KDAPKELLOMLE KDAPKELLOMLE	[]
PhS3 PhS4 PhS5	GATVKFKYKGEEKEVDISK GATVKFKYKGEEKEVDISK	I K K V W R V G K M I I K K V W R V G K M I	S F T Y D E G S F T Y D E G	GGKTGRGAVSE GGKTGRGAVSE	KDAPKELLQMLE KDAPKELLQMLE	
PhS6 PhS7	GATVKFKYKGEEKEVDISK	SKIKKVWRVGKMI	SF	TYDEGGGKTGRGAVSE	EKDAPKELLQMLE	
Pfi	059	88	χ _θ	. 088		_
DeepVent Hybrid_design HyS1 Hyb2	KQKKN					
Hyb3 Hys4 Phs1	KOKKIN KOKKN KOKKIN					
PhS4 PhS5	KO K K N KO K K N					
PhS7	KOKK					